RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/548,404_

Source: _PCT/10_

Date Processed by STIC: _9/21/05_

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PCT

RAW SEQUENCE LISTING   DATE: 09/21/2005
PATENT APPLICATION: US/10/548,404   TIME: 16:58:40

Input Set : **A:\PTO.KD.txt**
Output Set: **N:\CRF4\09212005\J548404.raw**

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   3 <110> APPLICANT: Bayer AG, BHC
   5 <120> TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with
   6       PHOSPHODIESTERASE 1B (PDE1B)
   8 <130> FILE REFERENCE: Le A 36 620
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/548,404
C--> 10 <141> CURRENT FILING DATE: 2005-09-08
  10 <160> NUMBER OF SEQ ID NOS: 5
  12 <170> SOFTWARE: PatentIn version 3.1
  14 <210> SEQ ID NO: 1
  15 <211> LENGTH: 2255
  16 <212> TYPE: DNA
  17 <213> ORGANISM: Homo sapiens
  19 <400> SEQUENCE: 1
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  22 gaggagtcgg attgcccgtc acccctggag ctgaagtcag cccccagcaa gaagatgtgg     120
  24 attaagcttc ggtctctgct gcgctacatg gtgaagcagt ggagaatgg ggagataaac     180
  26 attgaggagc tgaagaaaaa tctggagtac acagcttctc tgctggaagc cgtctacata     240
  28 gatgagacac ggcaaatctt ggacacggag gacgagctgc aggagctgcg gtcagatgcc     300
  30 gtgccttcgg aggtgcggga ctggctggcc tccaccttca cccagcaggc ccgggccaaa     360
  32 ggccgccgag cagaggagaa gcccaagttc cgaagcattg tgcacgctgt gcaggctggg     420
  34 atcttcgtgg aacggatgtt ccggagaaca tacacctctg tgggccccac ttactctact     480
  36 gcggttctca actgtctcaa gaacctggat ctctggtgct tgatgtctt ttccttgaac     540
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  44 cagacagtcc attgcttctt gctccgcaca gggatggtgc actgcctgtc ggagattgag     780
  46 ctcctggcca tcatctttgc tgcagctatc catgattatg agcacacggg cactaccaac     840
  48 agcttccaca tccagaccaa gtcagaatgt gccatcgtgt acaatgatcg ttcagtgctg     900
  50 gagaatcacc acatcagctc tgttttccga ttgatgcagg atgatgagat gaacattttc     960
  52 atcaacctca ccaaggatga gtttgtagaa ctccgagccc tggtcattga gatggtgttg    1020
  54 gccacagaca tgtcctgcca tttccagcaa gtgaagacca tgaagacagc cttgcaacag    1080
  56 ctggagagga ttgacaagcc caaggccctg tctctactgc tccatgctgc tgacatcagc    1140
  58 cacccaacca agcagtggtt ggtccacagc cgttggacca aggccctcat ggaggaattc    1200
  60 ttccgtcagg gtgacaagga ggcagagttg gcctgccct tttctccact ctgtgaccgc    1260
  62 acttccactc tagtggcaca gtctcagata gggttcatcg acttcattgt ggagcccaca    1320
  64 ttctctgtgc tgactgacgt ggcagagaag agtgttcagc ccctggcgga tgaggactcc    1380
  66 aagtctaaaa accagcccag cttttcagtgg cgccagccct ctctggatgt ggaagtggga    1440
  68 gaccccaacc ctgatgtggt cagctttcgt tccacctggg tcaagcgcat tcaggagaac    1500
  70 aagcagaaat ggaaggaacg ggcagcaagt ggcatcacca accagatgtc cattgacgag    1560
  72 ctgtccccct gtgaagaaga ggccccccca tccctgccg aagatgaaca caaccagaat    1620
  74 gggaatctgg attagccctg gggctggccc aggtcttcat tgagtccaaa gtgtttgatg    1680
  76 tcatcagcac catccatcag gactggctcc cccatctgct ccaagggagc gtggtcgtgg    1740
  78 aagaaacaac ccacctgaag gccaaatgcc agagatttgg ggttggggaa agggcccctc    1800
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80 cccacctgac acccactggg gtgcacttta atgttccggc agcaagactg gggaacttca  1860
82 ggctcccagt ggtcactgtg cccatccctc agcctctgga ttctcttcat ggccaggtgg  1920
84 ctgccaggga gcggggagct tcctggaggc ttcccagggc cttggggaag ggtcagagat  1980
86 gccagccccc tgggacctcc cccatccttt ttgcctccaa gtttctaagc aatacatttt  2040
88 gggggttccc tcagccccccc accccagatc ttagctggca ggtctgggtg cccctttcc  2100
90 tcccctggga agggctggaa taggatagaa agctgggggt tttcagagcc ctatgtgtgg  2160
92 ggaggggagt ggattccttc agggcatggt acctttctag gatctgggaa tggggtggag  2220
94 aggacatcct cttcacccca gaattgcggg aattc                             2255
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97 <210> SEQ ID NO: 2
98 <211> LENGTH: 536
99 <212> TYPE: PRT
100 <213> ORGANISM: Homo sapiens
102 <400> SEQUENCE: 2

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108 Cys Pro Ser Pro Leu Glu Leu Lys Ser Ala Pro Ser Lys Lys Met Trp
109             20                  25                  30
112 Ile Lys Leu Arg Ser Leu Leu Arg Tyr Met Val Lys Gln Leu Glu Asn
113         35                  40                  45
116 Gly Glu Ile Asn Ile Glu Glu Leu Lys Lys Asn Leu Glu Tyr Thr Ala
117     50                  55                  60
120 Ser Leu Leu Glu Ala Val Tyr Ile Asp Glu Thr Arg Gln Ile Leu Asp
121 65                  70                  75                  80
124 Thr Glu Asp Glu Leu Gln Glu Leu Arg Ser Asp Ala Val Pro Ser Glu
125             85                  90                  95
128 Val Arg Asp Trp Leu Ala Ser Thr Phe Thr Gln Gln Ala Arg Ala Lys
129             100                 105                 110
132 Gly Arg Arg Ala Glu Glu Lys Pro Lys Phe Arg Ser Ile Val His Ala
133         115                 120                 125
136 Val Gln Ala Gly Ile Phe Val Glu Arg Met Phe Arg Arg Thr Tyr Thr
137     130                 135                 140
140 Ser Val Gly Pro Thr Tyr Ser Thr Ala Val Leu Asn Cys Leu Lys Asn
141 145                 150                 155                 160
144 Leu Asp Leu Trp Cys Phe Asp Val Phe Ser Leu Asn Gln Ala Ala Asp
145             165                 170                 175
148 Asp His Ala Leu Arg Thr Ile Val Phe Glu Leu Leu Thr Arg His Asn
149             180                 185                 190
152 Leu Ile Ser Arg Phe Lys Ile Pro Thr Val Phe Leu Met Ser Phe Leu
153         195                 200                 205
156 Asp Ala Leu Glu Thr Gly Tyr Gly Lys Tyr Lys Asn Pro Tyr His Asn
157     210                 215                 220
160 Gln Ile His Ala Ala Asp Val Thr Gln Thr Val His Cys Phe Leu Leu
161 225                 230                 235                 240
164 Arg Thr Gly Met Val His Cys Leu Ser Glu Ile Glu Leu Leu Ala Ile
165             245                 250                 255
168 Ile Phe Ala Ala Ala Ile His Asp Tyr Glu His Thr Gly Thr Thr Asn
169             260                 265                 270
172 Ser Phe His Ile Gln Thr Lys Ser Glu Cys Ala Ile Val Tyr Asn Asp
173         275                 280                 285
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176 Arg Ser Val Leu Glu Asn His His Ile Ser Ser Val Phe Arg Leu Met
177     290                 295             300
180 Gln Asp Asp Glu Met Asn Ile Phe Ile Asn Leu Thr Lys Asp Glu Phe
181 305                 310             315             320
184 Val Glu Leu Arg Ala Leu Val Ile Glu Met Val Leu Ala Thr Asp Met
185             325             330             335
188 Ser Cys His Phe Gln Gln Val Lys Thr Met Lys Thr Ala Leu Gln Gln
189             340             345             350
192 Leu Glu Arg Ile Asp Lys Pro Lys Ala Leu Ser Leu Leu Leu His Ala
193         355             360             365
196 Ala Asp Ile Ser His Pro Thr Lys Gln Trp Leu Val His Ser Arg Trp
197     370             375             380
200 Thr Lys Ala Leu Met Glu Glu Phe Phe Arg Gln Gly Asp Lys Glu Ala
201 385                 390             395                 400
204 Glu Leu Gly Leu Pro Phe Ser Pro Leu Cys Asp Arg Thr Ser Thr Leu
205             405             410             415
208 Val Ala Gln Ser Gln Ile Gly Phe Ile Asp Phe Ile Val Glu Pro Thr
209             420             425             430
212 Phe Ser Val Leu Thr Asp Val Ala Glu Lys Ser Val Gln Pro Leu Ala
213         435             440             445
216 Asp Glu Asp Ser Lys Ser Lys Asn Gln Pro Ser Phe Gln Trp Arg Gln
217     450             455             460
220 Pro Ser Leu Asp Val Glu Val Gly Asp Pro Asn Pro Asp Val Val Ser
221 465             470             475                 480
224 Phe Arg Ser Thr Trp Val Lys Arg Ile Gln Glu Asn Lys Gln Lys Trp
225             485             490             495
228 Lys Glu Arg Ala Ala Ser Gly Ile Thr Asn Gln Met Ser Ile Asp Glu
229         500             505             510
232 Leu Ser Pro Cys Glu Glu Glu Ala Pro Pro Ser Pro Ala Glu Asp Glu
233         515             520             525
236 His Asn Gln Asn Gly Asn Leu Asp
237     530             535
240 <210> SEQ ID NO: 3
241 <211> LENGTH: 19
242 <212> TYPE: DNA
243 <213> ORGANISM: artificial sequence
245 <220> FEATURE:
246 <223> OTHER INFORMATION: forward primer
248 <400> SEQUENCE: 3
249 tgtggaagtg ggagacccc                                            19
252 <210> SEQ ID NO: 4
253 <211> LENGTH: 19
254 <212> TYPE: DNA
255 <213> ORGANISM: artificial sequence
257 <220> FEATURE:
258 <223> OTHER INFORMATION: reverse primer
260 <400> SEQUENCE: 4
261 ctgaatgcgc ttgacccag                                            19
264 <210> SEQ ID NO: 5
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265 <211> LENGTH: 27
266 <212> TYPE: DNA
267 <213> ORGANISM: artificial sequence
269 <220> FEATURE:
270 <223> OTHER INFORMATION: probe
272 <400> SEQUENCE: 5
273 accctgatgt ggtcagcttt cgttcca   27

VERIFICATION SUMMARY   DATE: 09/21/2005
PATENT APPLICATION: **US/10/548,404**   TIME: 16:58:41

Input Set : **A:\PTO.KD.txt**
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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date